

FIG. 1A

FIG. 1B

FIG. 1C

FIG. 1D

FIG. 1E

FIG. 1F

FIG. 1

1 GGATCCTGGT CGCGAGCGCG CCGCCCAGCC ACCTGCCGGC GCGCCCCGCC
 GGGACCGCTC GAGGACGCCT CGCGAAGGCT CTAGGGGCTG TATCTTCAAG
 101 AGTCTACGCC CCTTTGTTGC AGTGCACAAA TTTCGGTGCT AGCTTCATGC
 "-35"
 TATCAGGCC CAGACGAGGA AGATTCACCG ^{*phaE*} TGAACGATAC GGCCAACAAG
 S/D V N D T A N K
 201 ACCAGCGACT GGCTGGACAT CCAACGCAAG TACTGGGAGA CCTGGTCGGA
 T S D W L D I Q R K Y W E T W S E
 GCTCGGCCGC AAGACCTTGG GTCTGGAGAA GACCCCGGCC AATCCTTGGG
 L G R E T L G L E F T P A N P W A
 301 CCGGCGCCCT CGATCATTGG TGGCAGACGG TCTCGCCCGC CGCCCCAAC
 G A L D H W W Q T V S P A A P N
 GACCTGGTTC GCGACTTCAT GGAGAAGCTC GCGAGCAGG GCAAGGCCTT
 D F V R D F M F K I A F Q G K A F
 401 CTTGGGCTC ACCGACTACT TCACGAAGGG CCTCGGCGGC AGTAGCGGTA
 F G L T D Y F I K G L G G S S G T
 CGCAGGGCTG GGACACCCTC TCGAAGACCA TCGACGACAT GCAAAAGGCC

FIG. 1A

501 TTCGCCAGCG GCCGGATCGA AGGCGACGAG ACCTTCCGCC GCCTGATGGC
 F A S G R I E G D E T F R R L M A

 CTTCTGGGAG ATGCCGCTCG ACAACTGGCA GCGCACCATG TCCTCGCTGT
 F W E M P L D N W Q R T M S S L S

 601 CCCCGGTGCC CGGCGACCTG CTGCGCAACA TGCCGCACGA CCAAGTCAGG
 P V P G D L L R N M P H D Q V R

 GACAGCGTCG ACCGCATCCT CTCGGCACCC GGGCTCGGCT ACACGCGCGA
 D S V D R I L S A P G I G Y T R E

 701 GGAGCAGGCC CGCTACCAGG ATCTGATCCG CCGCTCGCTG GAGTACCACT
 E Q A R Y Q D L I R R S L E Y Q S

 CGGCCCTGAA CGAATACAAC GGCTTCTTCG GCCAGCTCGG TGTCAAGTCC
 A L N E Y N G F F G Q L G V K S

 801 CTCGAGCGGA TGCGCGCCTT CCTGCAGGGA CAGGCCGAGA AGGGCGTCGC
 L E R M R A F L Q G Q A E K G V A

 CATCGAGTCG GCGCGCACCC TCTACGACGC CTGGGTCTGGC TGCTGCGAAG
 I F S A R T I Y D A W V G C C E E

 901 AGGTCATGC CGAGGAGGTC AGCTCGGAG ACTACGGCA CATCACGGC
 V Y A E E V S S A D Y A H I H G

 CGCCTCGTCA ACGCCCAGAT GGCCCTCAAG CAGCGCATGT CGACCATGGT
 R I V N A Q M A I K Q R M S I M V

FIG. 1B

1001 CGACGAGGTC CTCGGCGCGA TGCCGCTGCC GACCCGCAGC GAGCTGCCGA
D E V L G A M P L P T R S E L R T

CGCTCCAGGA TCGGCTCCAG GAGTCGCCCG GCGAGGGCAA GCGCCAGCGC
L Q D R L Q E S R G E G K R Q R

1101 CAAGAGATCG AGACGCTGAA GCGGCAGGTC GCGGCCTTGG CCGGCGGGCG
Q F I E T L K R Q V A A L A G G A

CCAGCCCGCG CCCGAGGCCT CCGCCGAGCC CAGCACCCGG CCCGCGCCGG
Q P A P Q A S A Q P S T R P A P A

1201 CGACGGCCCC GCGGGCGAGC GCGGGGCCCA AGCGCAGCAC CACGACCCGC
T A P A A S A A P K R S T T T R

CGCAAGACCA CCAAGCCCAC CACCGGCCAG TGATGTGGG CGCCCGTCCA
R E T T K P T T G Q *

1301 TCGCCACCAG *phaC*
GAGAGAGTGC $\xrightarrow{\quad}$ CGTGTCCCCA TTCCCGATCG ACATCCGGCC
S/D V S P F P I D I R P

CGACAAGCTG ACCGAGGAGA TGCTGGAGTA CAGCCGCAAG CTCGGCGAGG
D K I T T T M L T Y S R K L G G

1401 GTATGCAGAA CCGCTCAAG GCGACCCAGA TCGACACAGG CGTCACCCCG
M Q N L L F A D Q I D T G V T P

AAGGACGTGG TCCACCGCGA GGACAAGCTG GTCTCTACG GCTACCGGGG

FIG. 1C

1501 CCGGGCGCAG GTGGCGACCC AGACGATCCC GCTGCTGATC GTCTACGCCC
P A Q V A T Q T I P L L I V Y A L

TCGTCAATCG GCCCTACATG ACCGACATCC AGGAGGATCG CTCGACGATC
V N R P Y M T D I Q E D R S T I

1601 AAGGGCCTGC TCGCCACCGG TCAGGACGTC TATCTGATCG ACTGGGGCTA
K G L L A T G Q D V Y L I D W G Y

CCCGGATCAG GCCGACCGGG CGCTGACCCT CGATGACTAC ATCAACGGCT
P D Q A D R A I T L D D Y I N G Y

1701 ACATCGACCG CTGCGTCGAC TACCTGCGCG AGACCCACGG CGTCGACCAG
I D R C V D Y L R E T H G V D Q

GTCAACCTGC TCGGGATCTG CCAGGGCGGG GCCTTCAGCC TCTGCTACAC
V N L L G I C Q G G A F S L C Y T

1801 GGCCCTGCAC TCCGAGAAGG TCAAAAACCT CGTCACCATG GTCACGCCGG
A L H S E K V K N L V T M V T P V

TCGACTTCCA GACCCCGGGC AACCTGCTCT CGGCCTGGGT CCAGAACGTC
D F Q T P G N I L S A W V Q N V

1901 GAGCTGAGC TGGCCGTCCA CACCATGGGC AACATCTCG GCGAATGCT
D V D L A V D I M G N I P G F I L

CAACTGGACC TTCCTGTCGC TCAAGCCCTT CAGCCTGACC GGCCAGAAGT
N W I F L S I K P F S I I G Q K Y

FIG. 1D

2001 ACGTCAACAT GGTCGACCTG CTCGACGAGG AGGACAAGGT CAAGAACTTC
V N M V D L L D D E D K V K N F

CTGCGGATGG AGAAGTGGAT CTTCGACAGC CCGGACCAGG CCGGCGAGAC
L R M E K W I F D S P D Q A G E T

2101 CTTCCGCCAG TTCATCAAGG ACTTCTACCA GCGCAACGGC TTCATCAACG
F R Q F I K D F Y Q R N G F I N G

GCGGCGTCCT GATCGGGGAT CAGGAGGTGG ACCTGCGCAA CATCCGCTGC
G V L I G D Q E V D L R N I R C

2201 CCGGTCCTGA ACATCTACCC GATGCAGGAC CACCTGGTGC CGCCGGATGC
P V L N I Y P M Q D H L V P P D A

CTCCAAGGCC CTGCGGGGAC TGACCTCCAG CGAGGACTAC ACGGAGCTCG
S K A L A G L T S S E D Y T E L A

2301 CCTTCCCCGG CGGGCACATC GGCATCTACG TCAGCGGCAA GGCGCAGGAA
F P G G H I G I Y V S G K A Q E

GGAGTCACCC CGGCGATCGG CCGCTGGCTG AACGAACGGG GCTGAGCCGG
G V T P A I G R W L N E R G *

2401 GTCGACCCAG CCGCTCGACG GCGCGGGCCG GCGGCATCGA AGGCCGCGCG

CGGGCGCCCA TGAGGCATCC GCGCGGCTGG CGGCCGCCCC CGGACCTTCG

FIG. 1E

2501 CCGCCGCACC CGCATCGCCC CCGCGGGCTGG CGTACAATGA CCGTCTTCGC

GAGCGAGCCC CGCATCGTCA ACGGAGGCTG CATGGGCGCC GACCACCAAC

2601 TGCTGGCCGC GTACGACGGG CTGGCCGAGA CCTACGACGC CCACCGCGGC

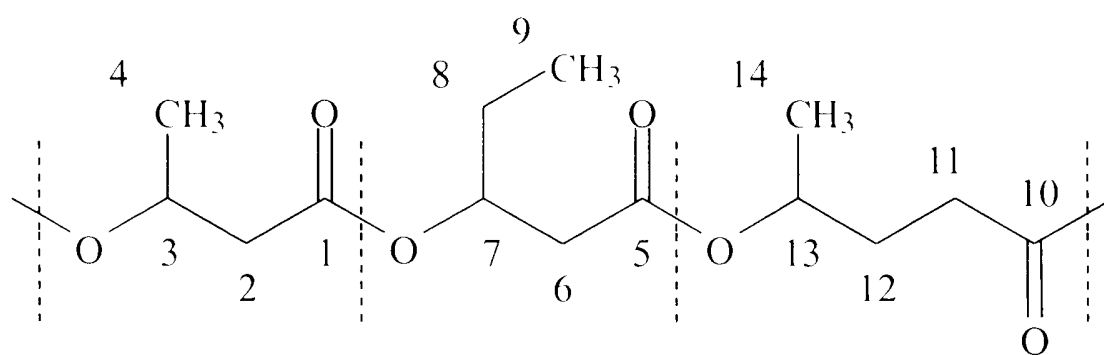
CTCTTCGACA TGGCGCCGT GCTCGAGGAC ATCTTCGCCC GCCTGCCGGC

2701 CTGCGGCACC CTCCTCGACC TCGGCTGCGG CGCCGGGGAG CCGTGCGCGC

GCGCCTTCCT CGACCGCGGC TGGCGGGTGA CCGGGGTGGA CTTCTGCCCG

2801 GCCATGCTCG CCCTCGCGGC GCGCTACGTC CCCGAGATGG AGCGGATCC

FIG. 1F



3HB

3HV

4HV

FIG. 2

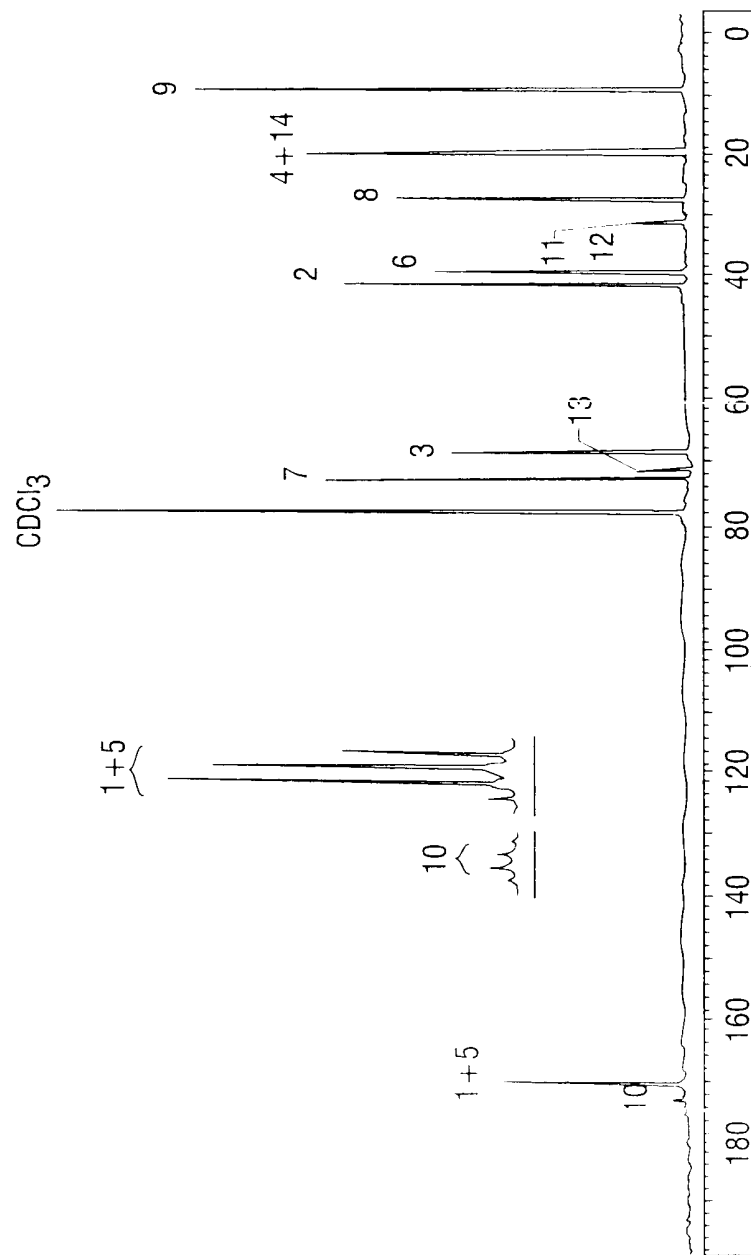


FIG. 3

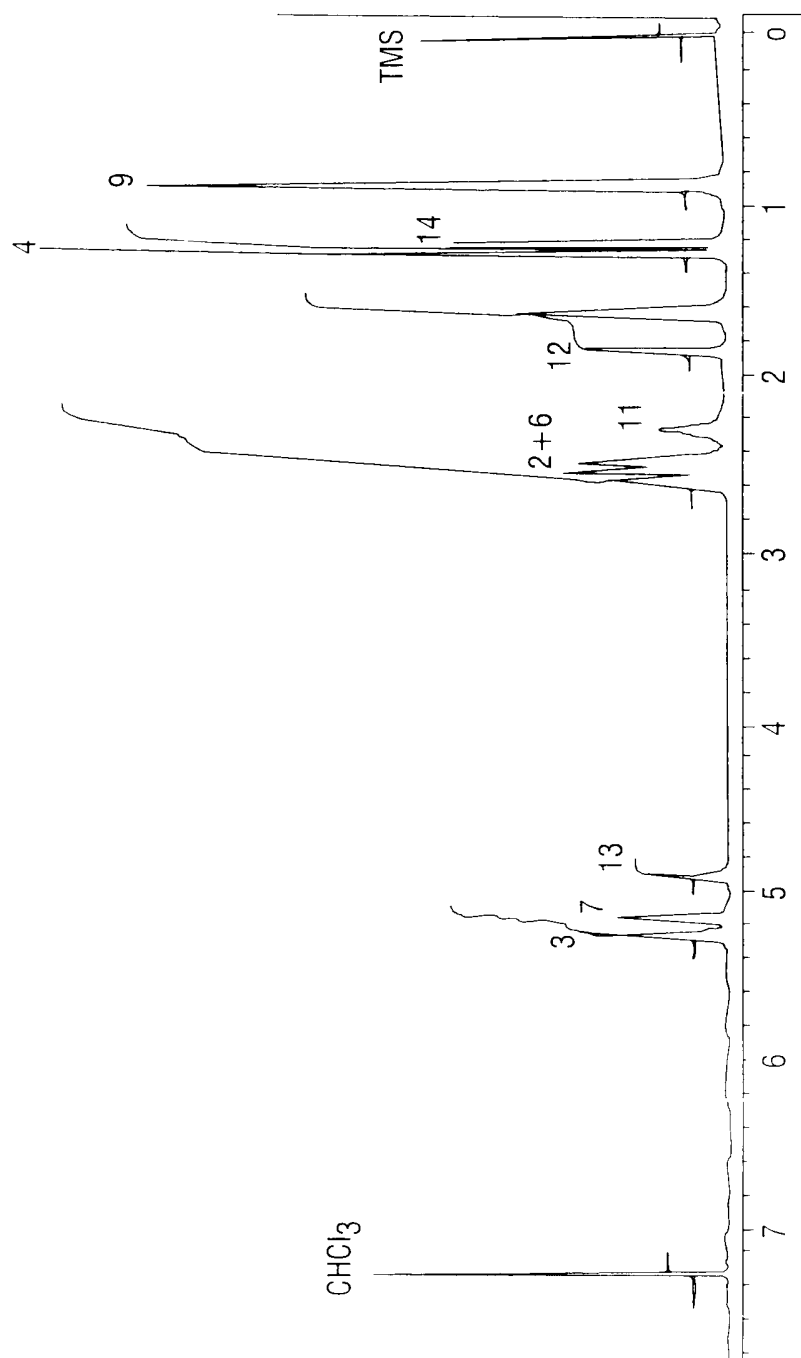


FIG. 4

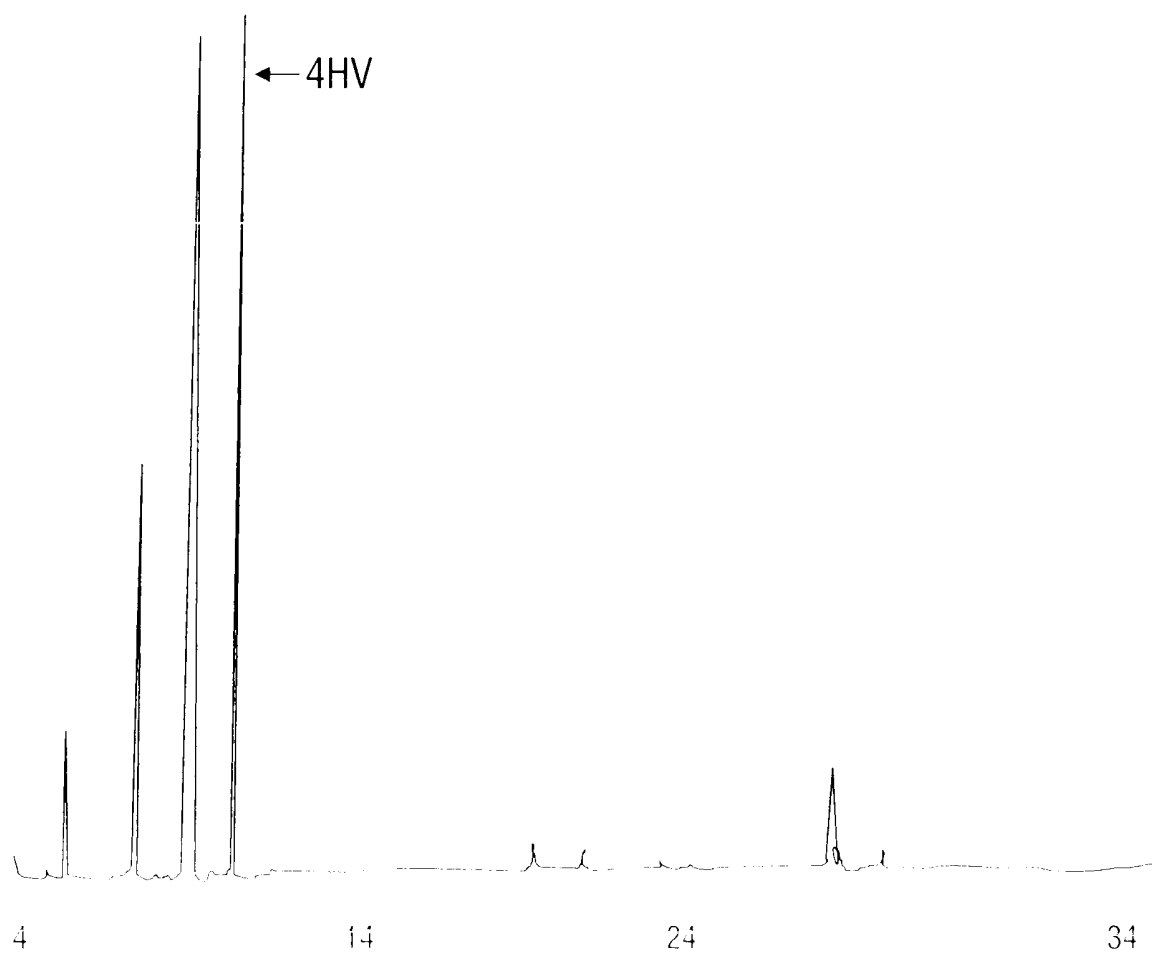


FIG. 5

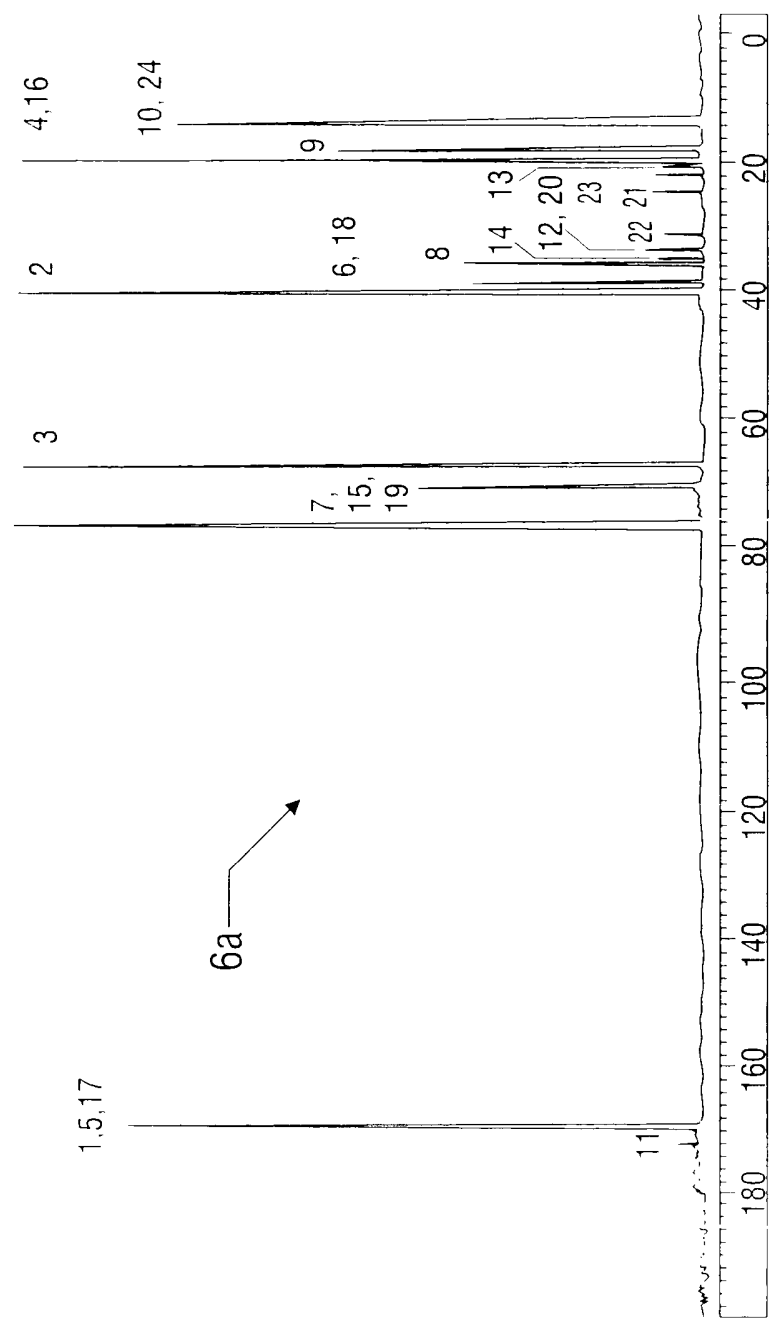


FIG. 6

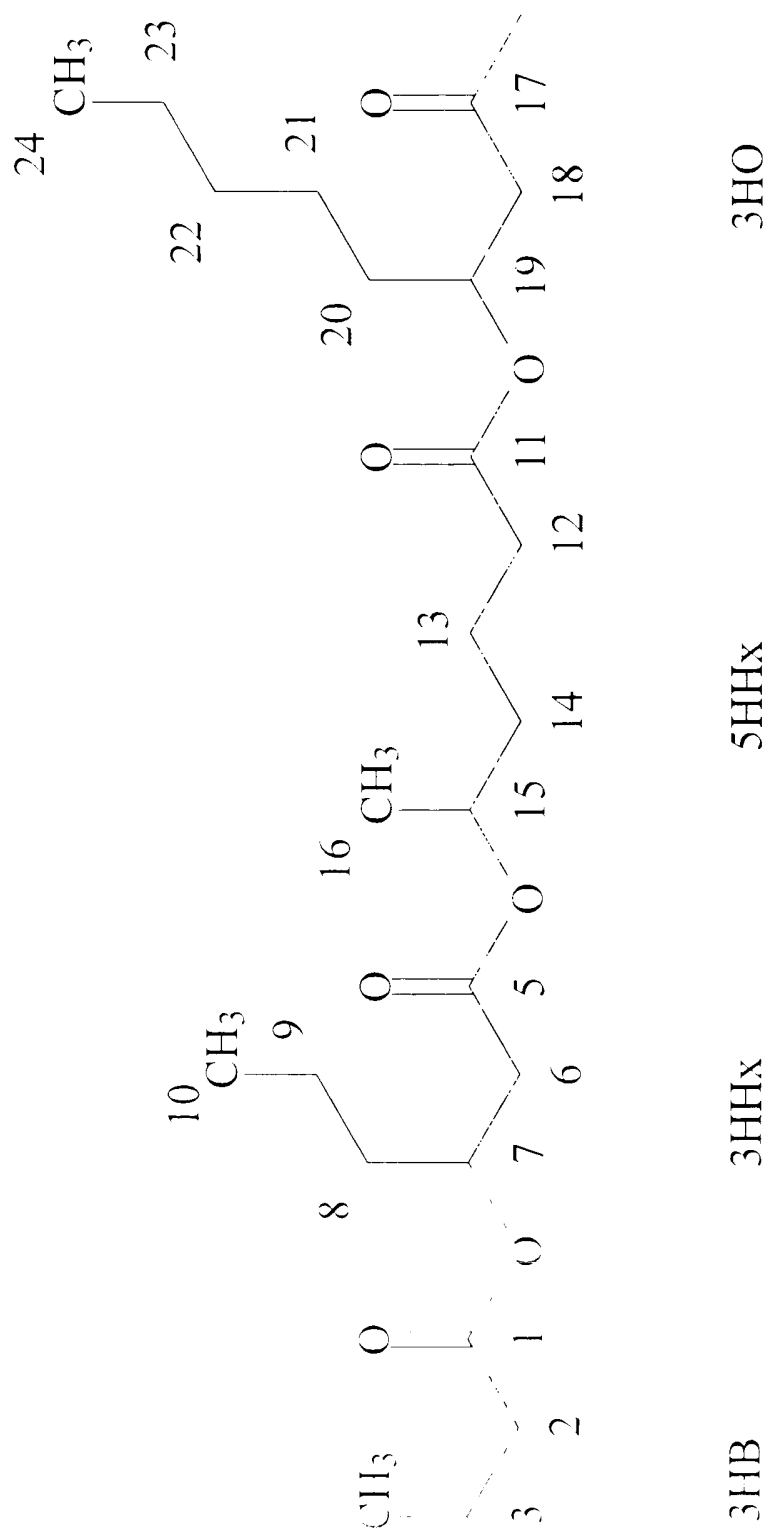


FIG. 6A

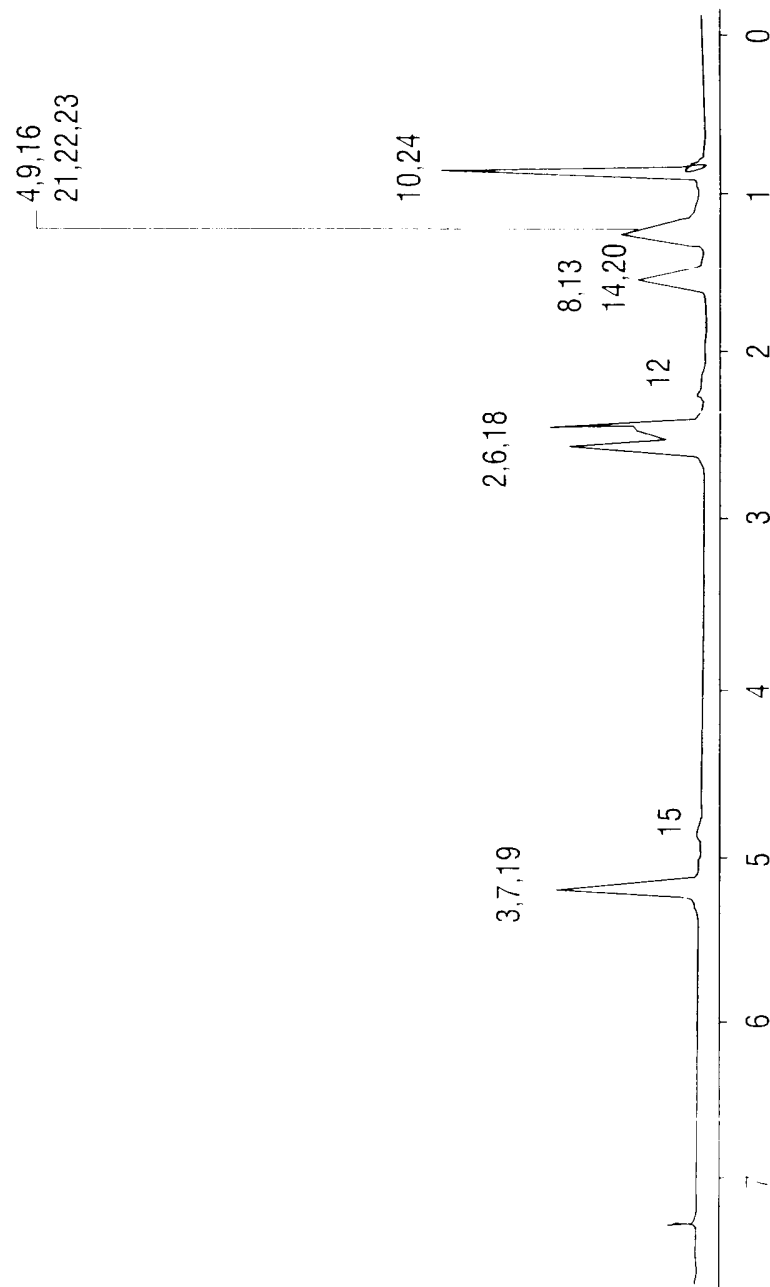


FIG. 7

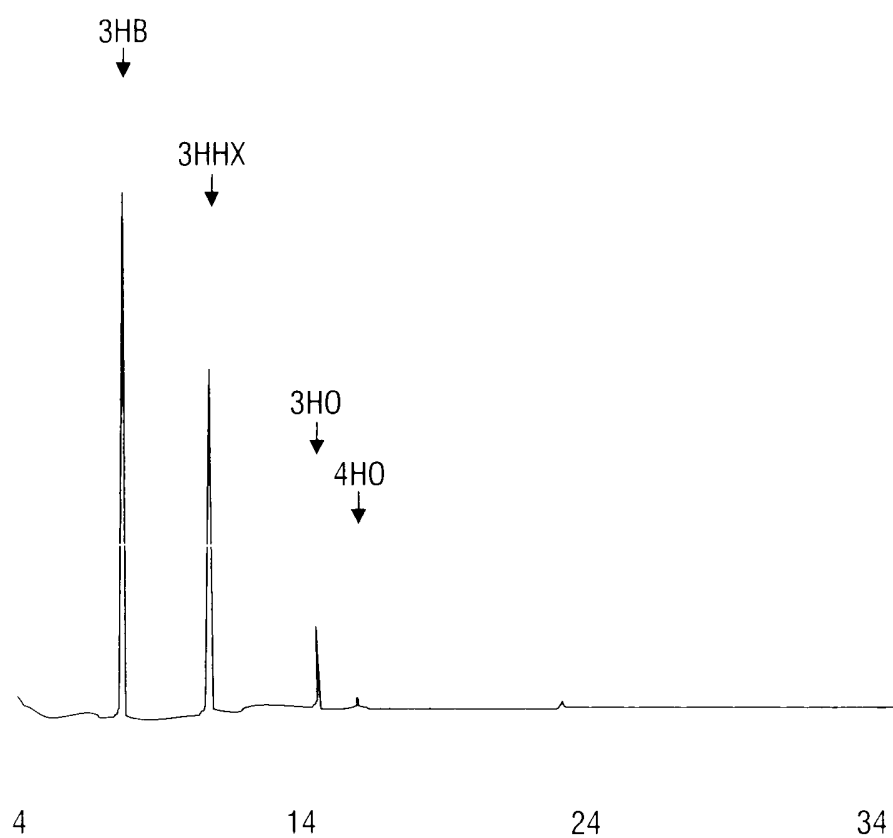


FIG. 8

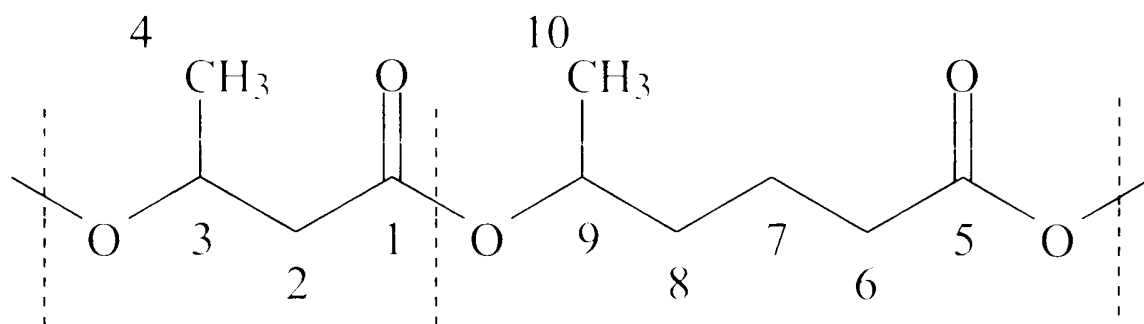


FIG. 9

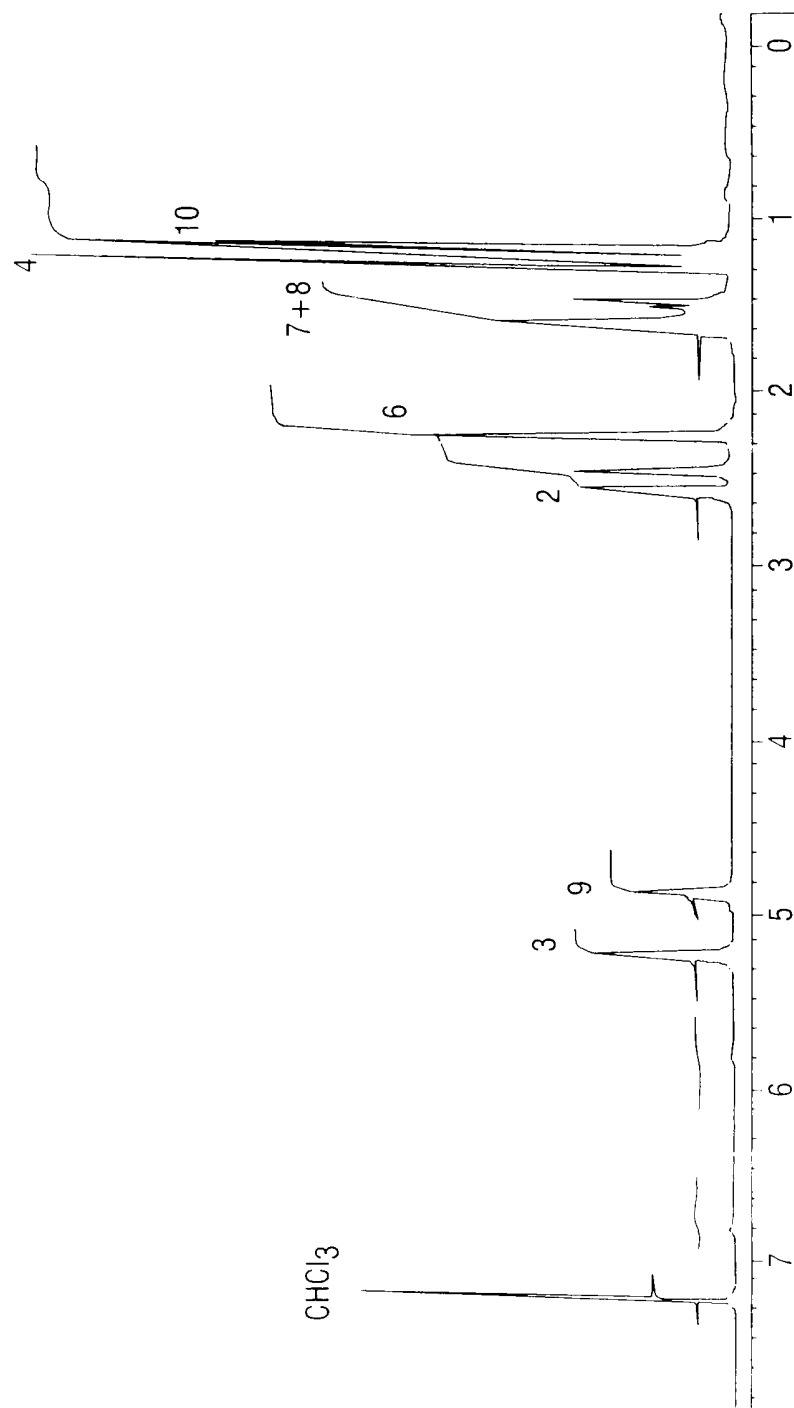


FIG. 10

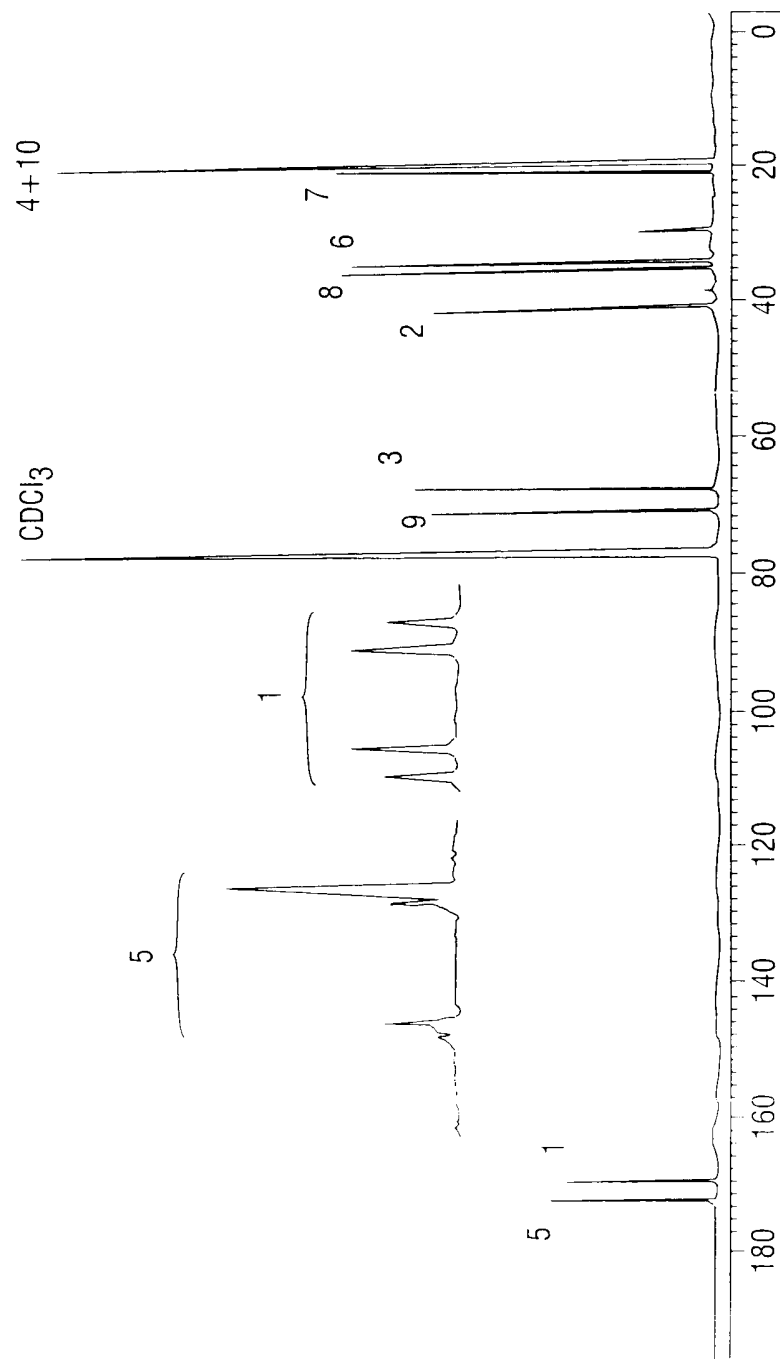


FIG. 11

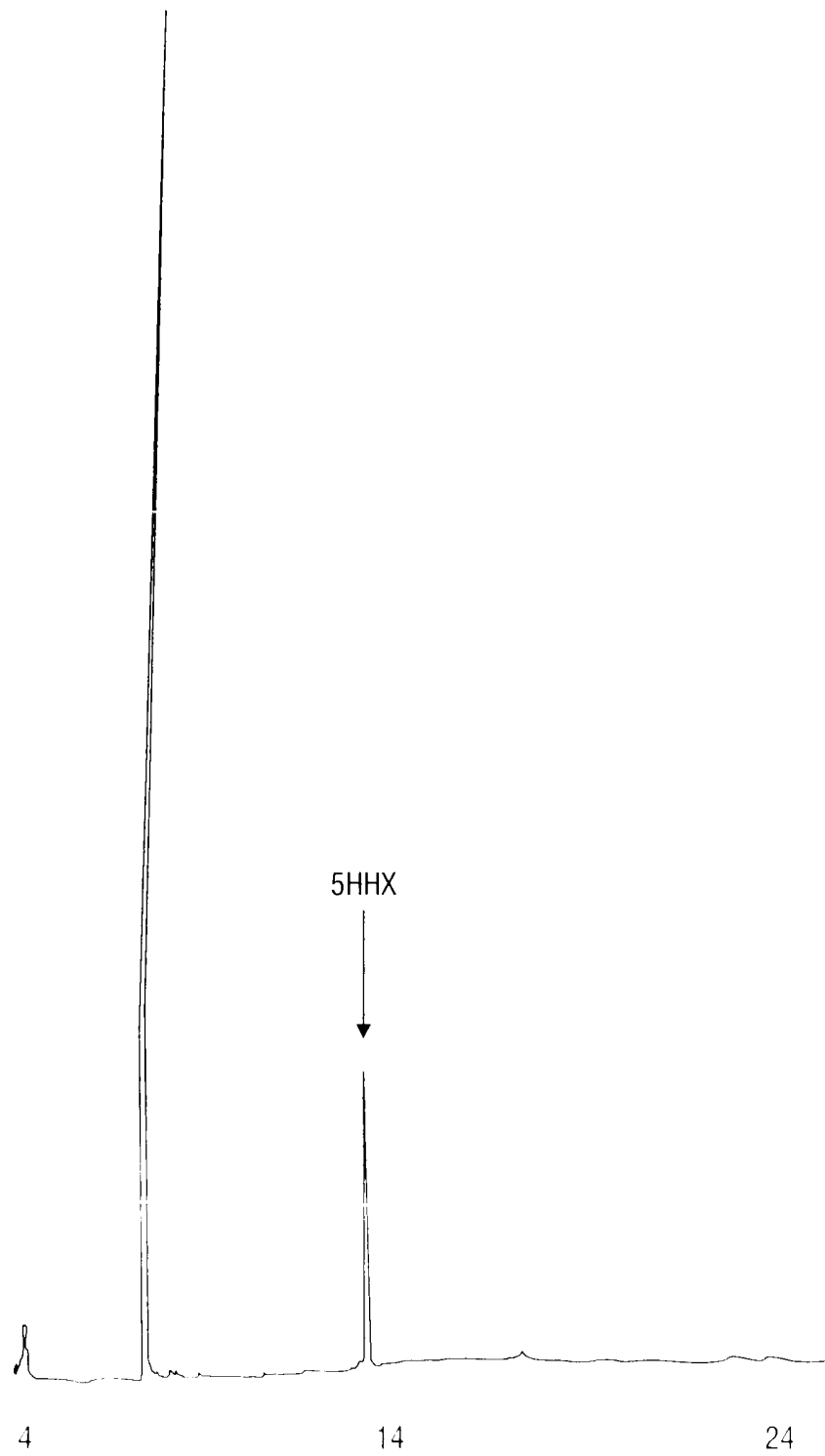


FIG. 12

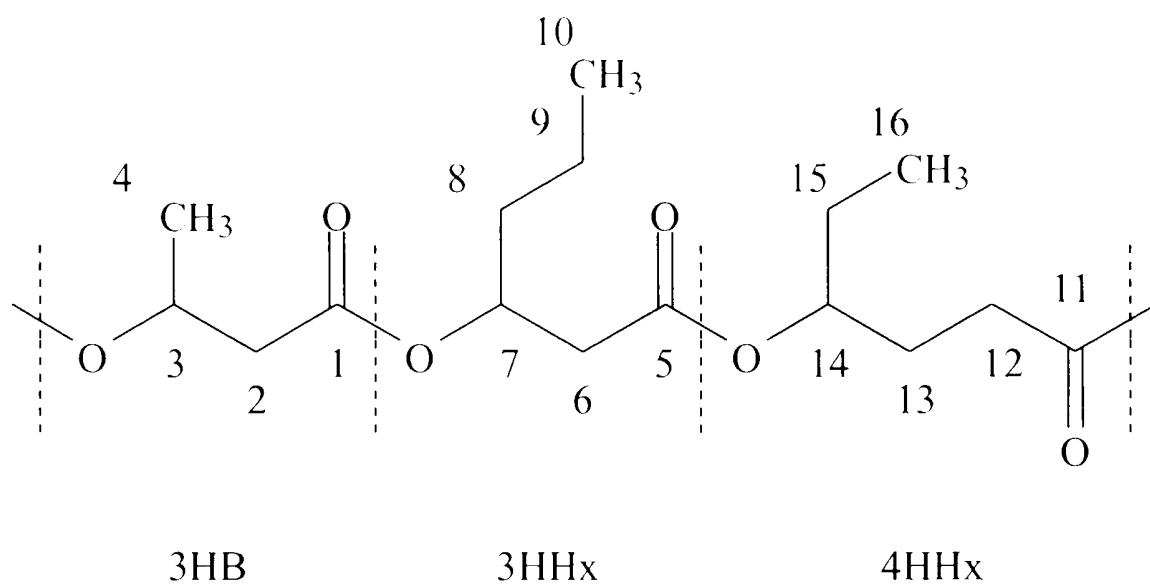


FIG. 13

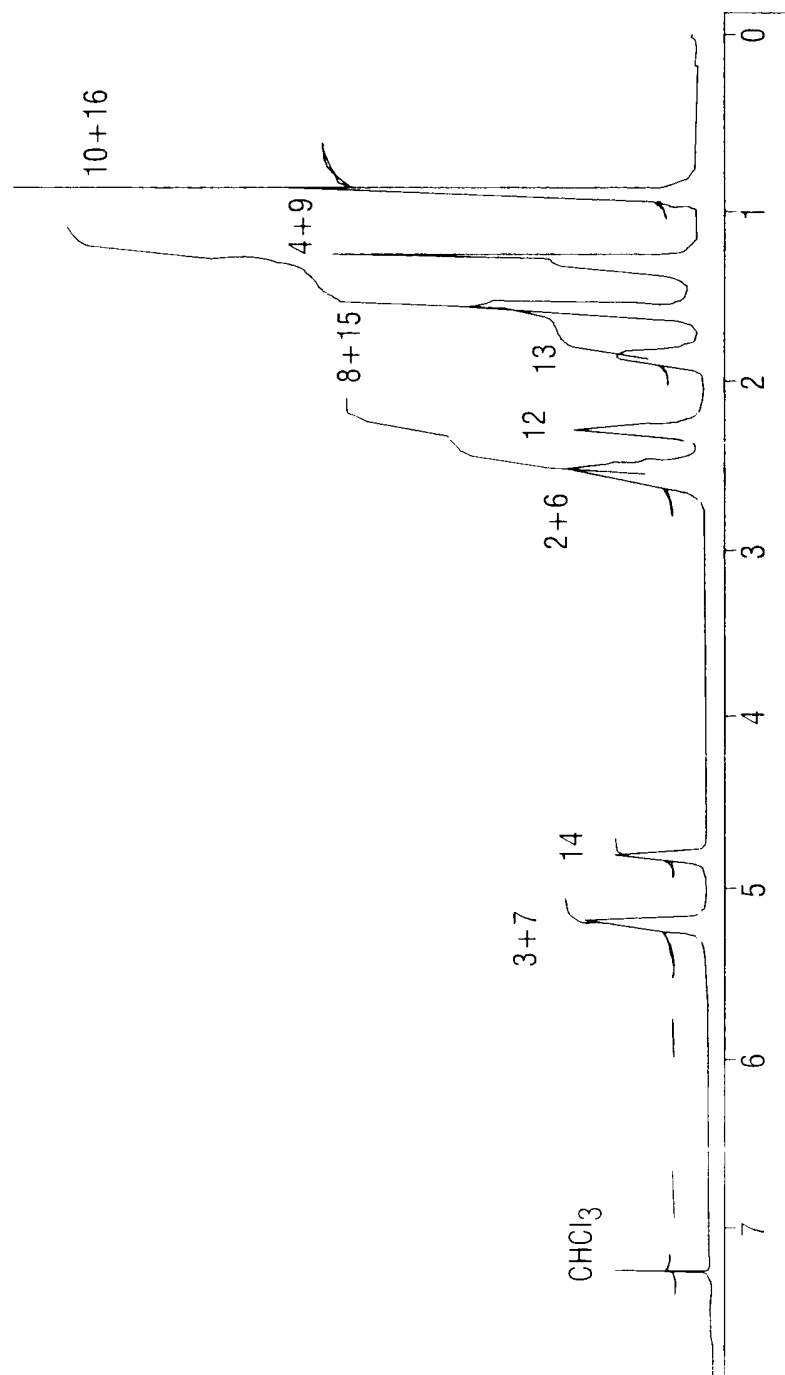


FIG. 14

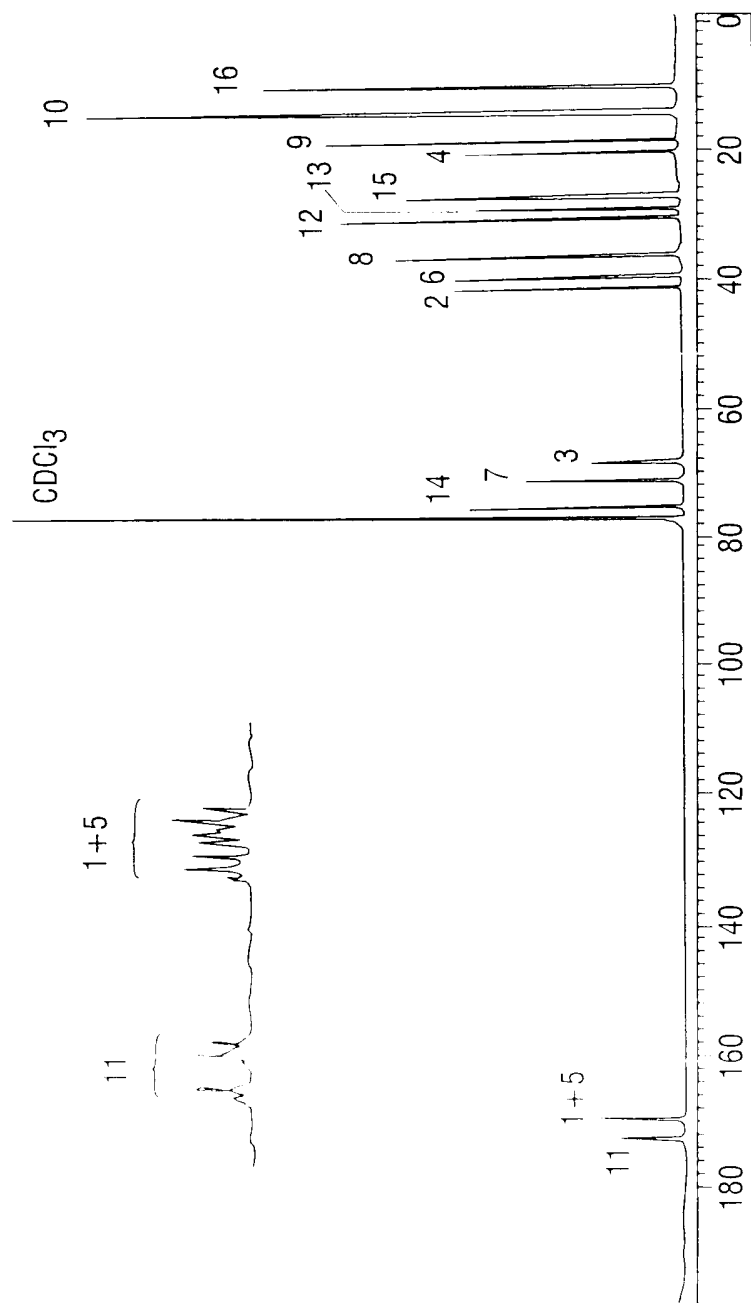


FIG. 15

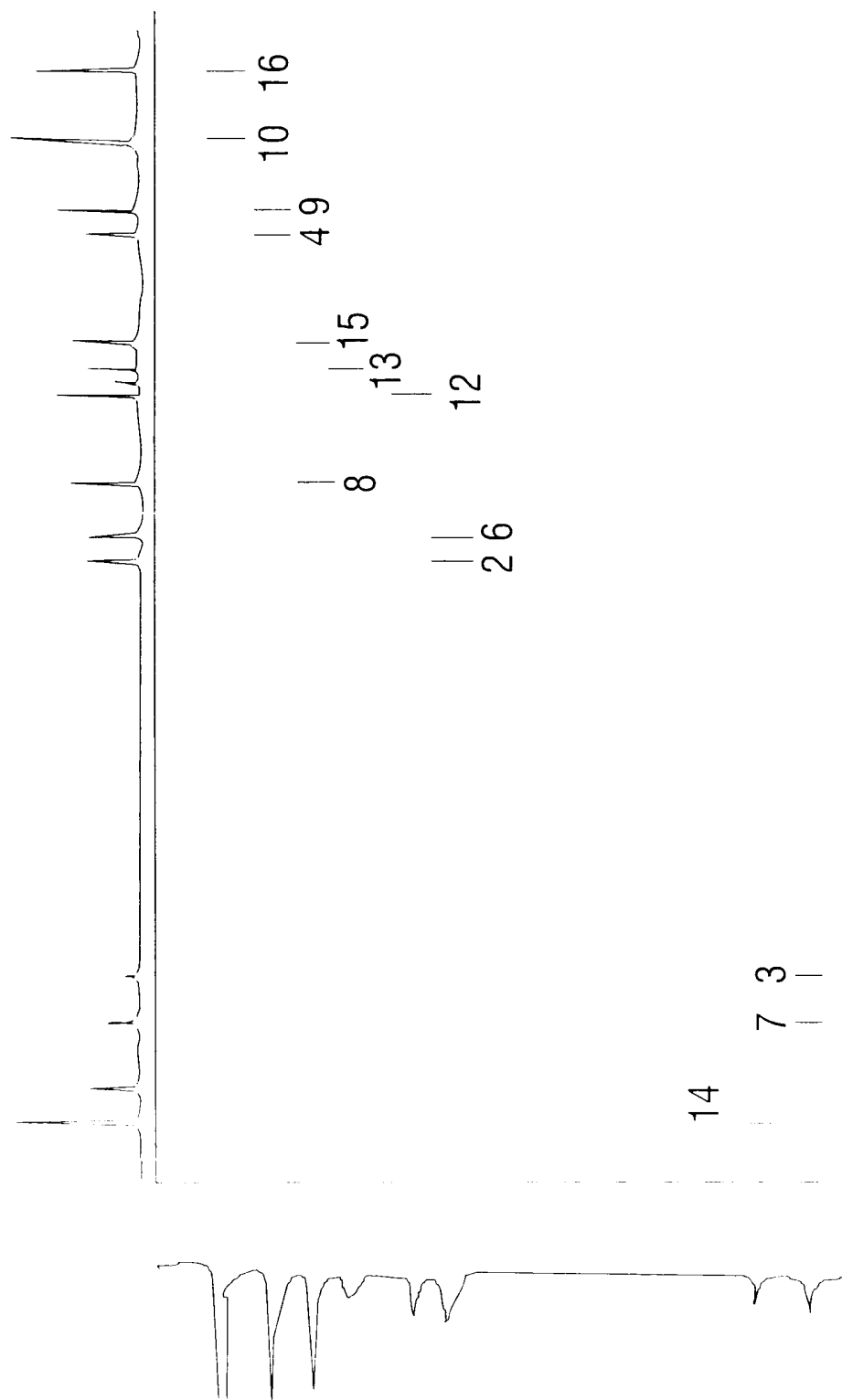


FIG. 16

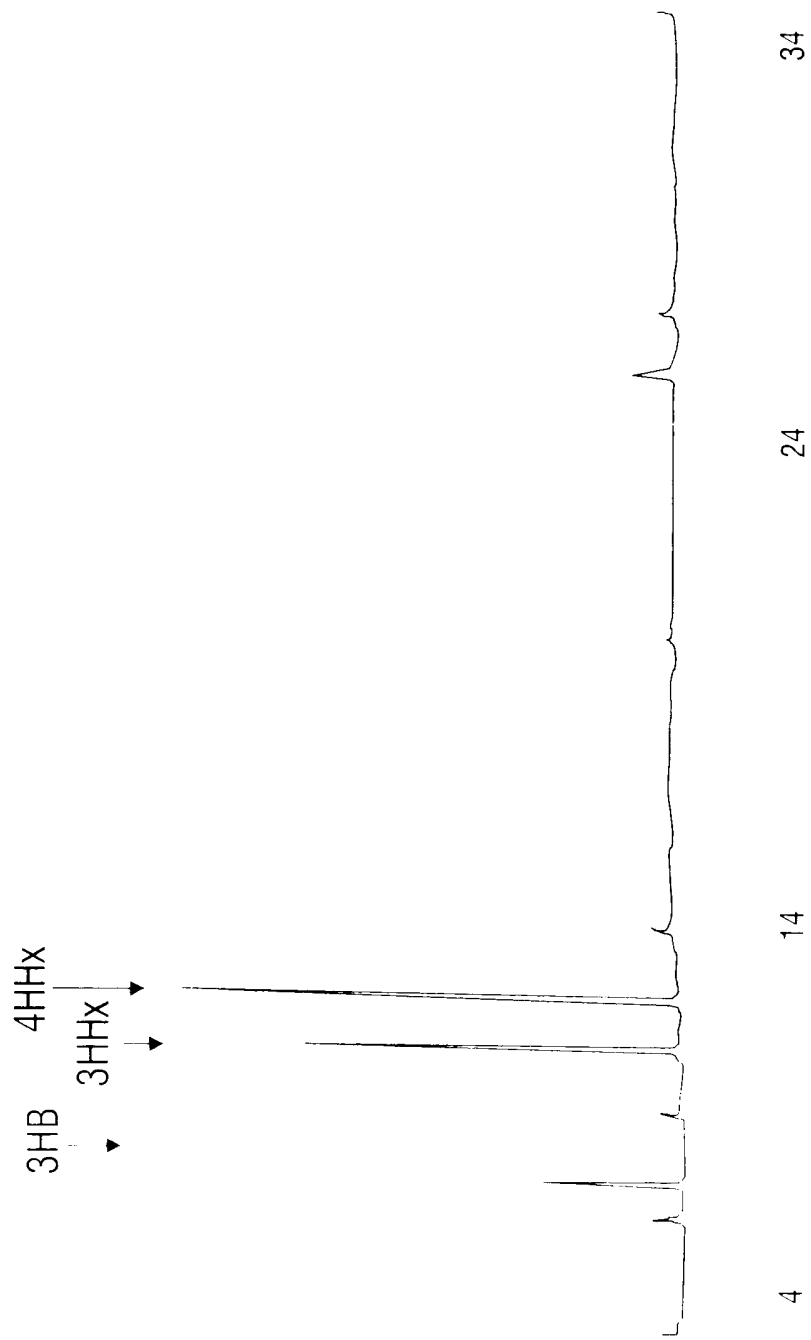


FIG. 17